FIG. 1A

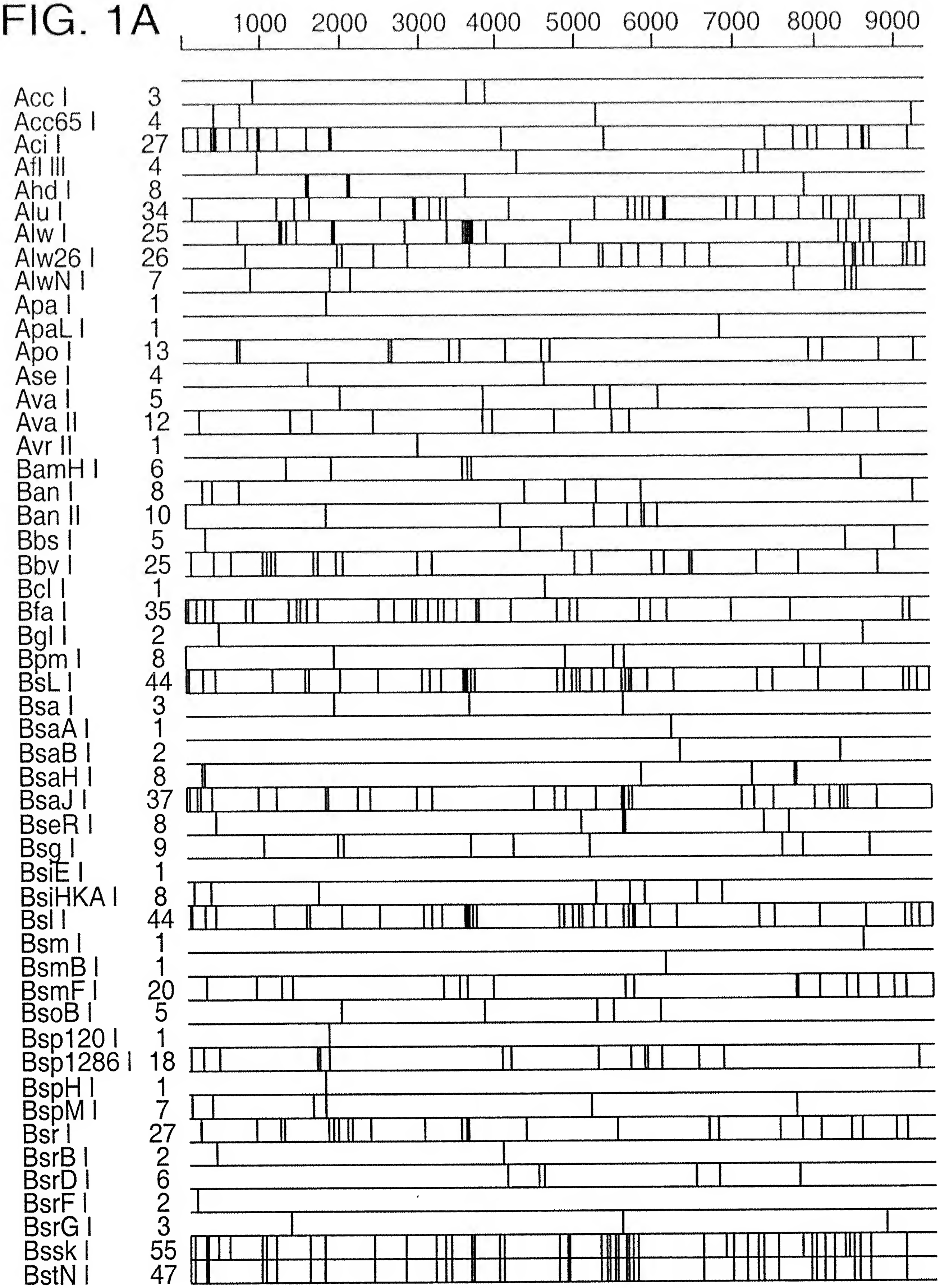

1000 2000 3000 4000 5000 6000 7000 8000 9000
Acc I 3
Acc65 I 4
Aci I 27
Afl III 4
Ahd I 8
Alu I 34
Alw I 25
Alw26 I 26
AlwN I 7
Apa I 1
ApaL I 1
Apo I 13
Ase I 4
Ava I 5
Ava II 12
Avr II 1
BamH I 6
Ban I 8
Ban II 10
Bbs I 5
Bbv I 25
Bcl I 1
Bfa I 35
Bgl I 2
Bpm I 8
BsL I 44
Bsa I 3
BsaA I 1
BsaB I 2
BsaH I 8
BsaJ I 37
BseR I 8
Bsg I 9
BsiE I 1
BsiHKA I 8
Bsl I 44
Bsm I 1
BsmB I 1
BsmF I 20
BsoB I 5
Bsp120 I 1
Bsp1286 I 18
BspH I 1
BspM I 7
Bsr I 27
BsrB I 2
BsrD I 6
BsrF I 2
BsrG I 3
Bssk I 55
BstN I 47

FIG. 1B

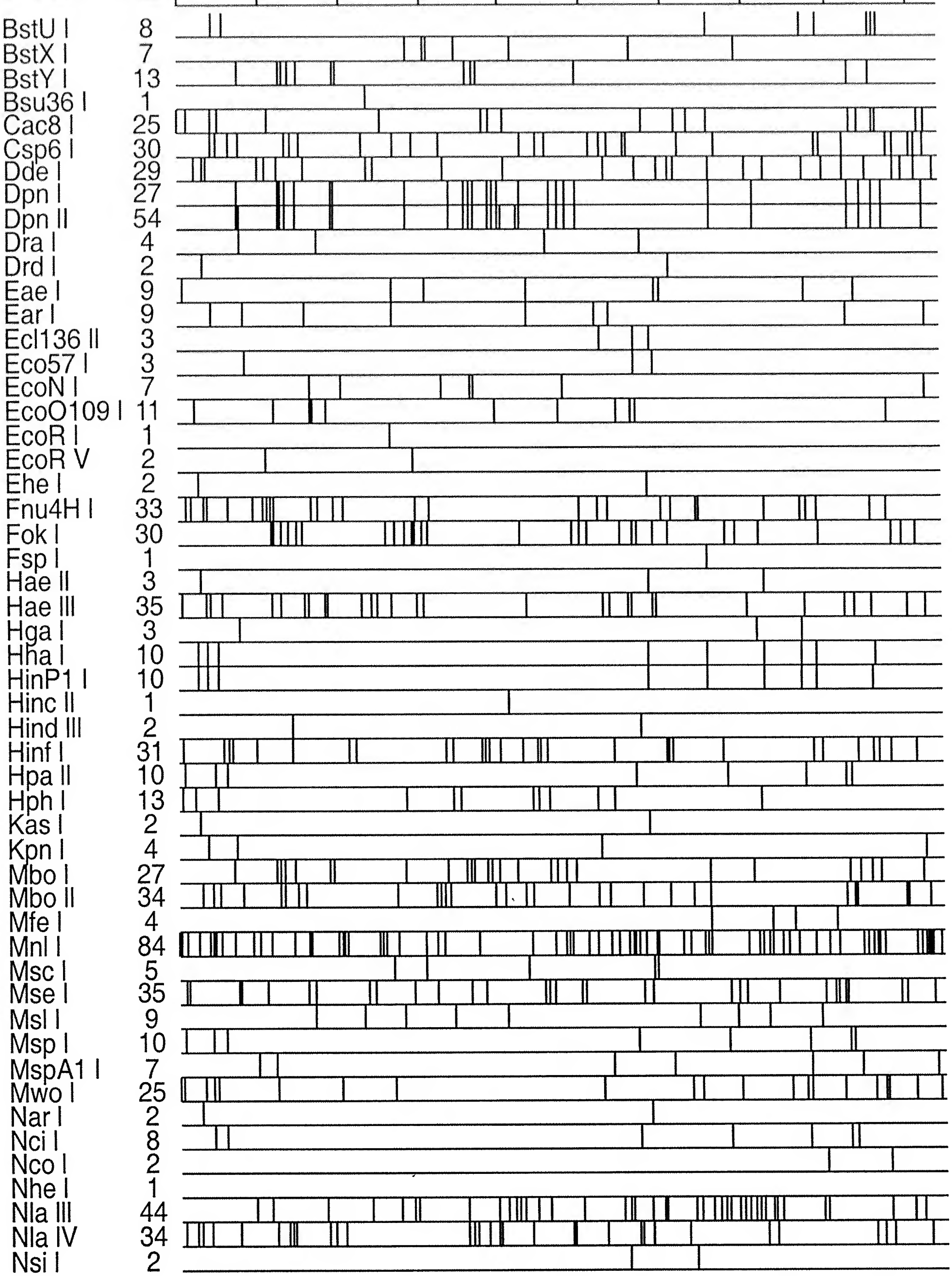

1000 2000 3000 4000 5000 6000 7000 8000 9000
BstU I 8
BstX I 7
BstY I 13
Bsu36 I 1
Cac8 I 25
Csp6 I 30
Dde I 29
Dpn I 27
Dpn II 54
Dra I 4
Drd I 2
Eae I 9
Ear I 9
Ecl136 II 3
Eco57 I 3
EcoN I 7
EcoO109 I 11
EcoR I 1
EcoR V 2
Ehe I 2
Fnu4H I 33
Fok I 30
Fsp I 1
Hae II 3
Hae III 35
Hga I 3
Hha I 10
HinP1 I 10
Hinc II 1
Hind III 2
Hinf I 31
Hpa II 10
Hph I 13
Kas I 2
Kpn I 4
Mbo I 27
Mbo II 34
Mfe I 4
Mnl I 84
Msc I 5
Mse I 35
Msl I 9
Msp I 10
MspA1 I 7
Mwo I 25
Nar I 2
Nci I 8
Nco I 2
Nhe I 1
Nla III 44
Nla IV 34
Nsi I 2

FIG. 1C

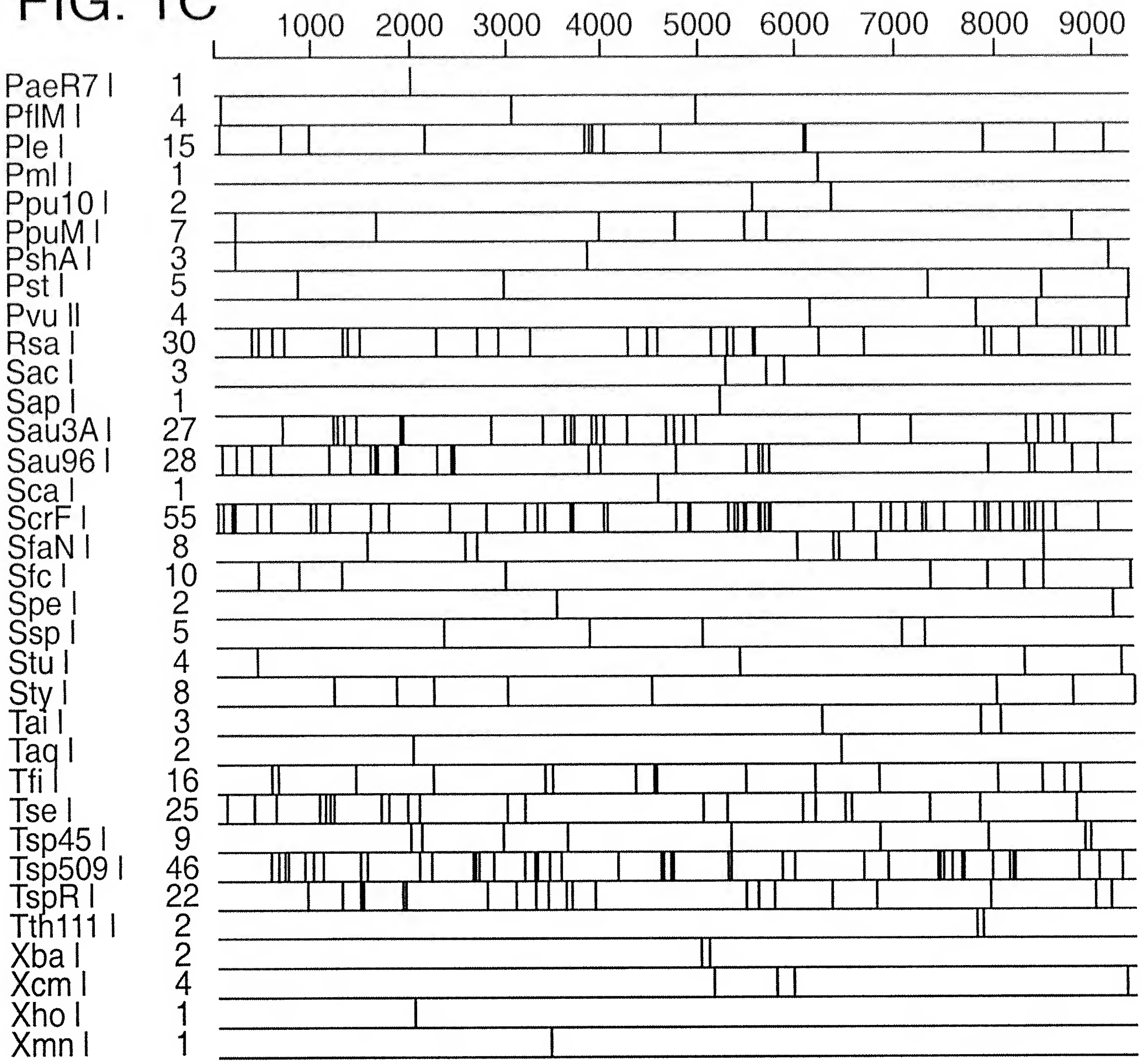

1000
2000
3000
4000
5000
6000
7000
8000
9000
PaeR7 I 1
PflM I 4
Ple I 15
Pml I 1
Ppu10 I 2
PpuM I 7
PshA I 3
Pst I 5
Pvu II 4
Rsa I 30
Sac I 3
Sap I 1
Sau3A I 27
Sau96 I 28
Sca I 1
ScrF I 55
SfaN I 8
Sfc I 10
Spe I 2
Ssp I 5
Stu I 4
Sty I 8
Tai I 3
Taq I 2
Tfi I 16
Tse I 25
Tsp45 I 9
Tsp509 I 46
TspR I 22
Tth111 I 2
Xba I 2
Xcm I 4
Xho I 1
Xmn I 1

FIG. 2A

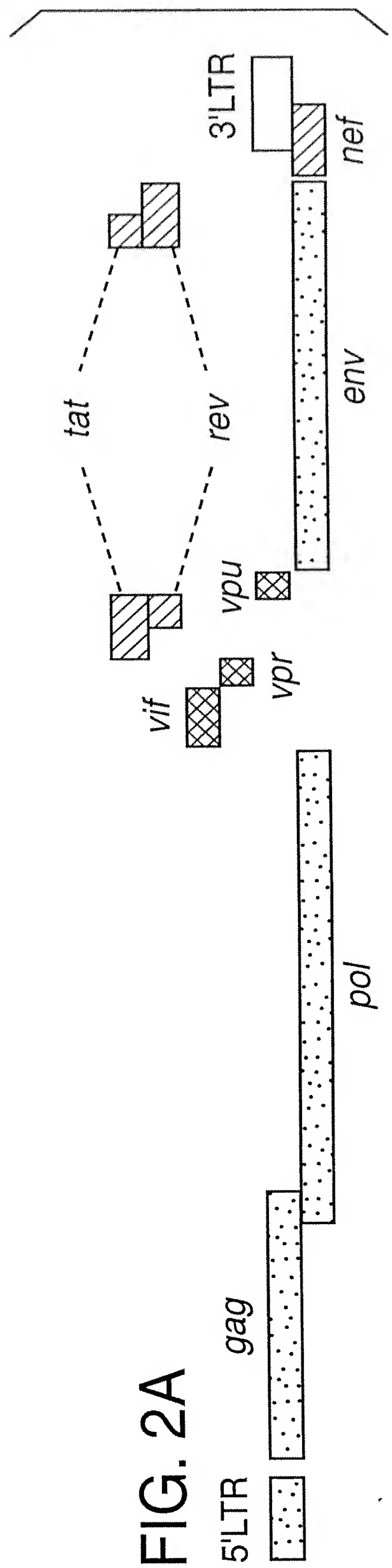

5'LTR
gag
pol
vif
vpr
vpu
tat
rev
env
nef
3'LTR

FIG. 2B

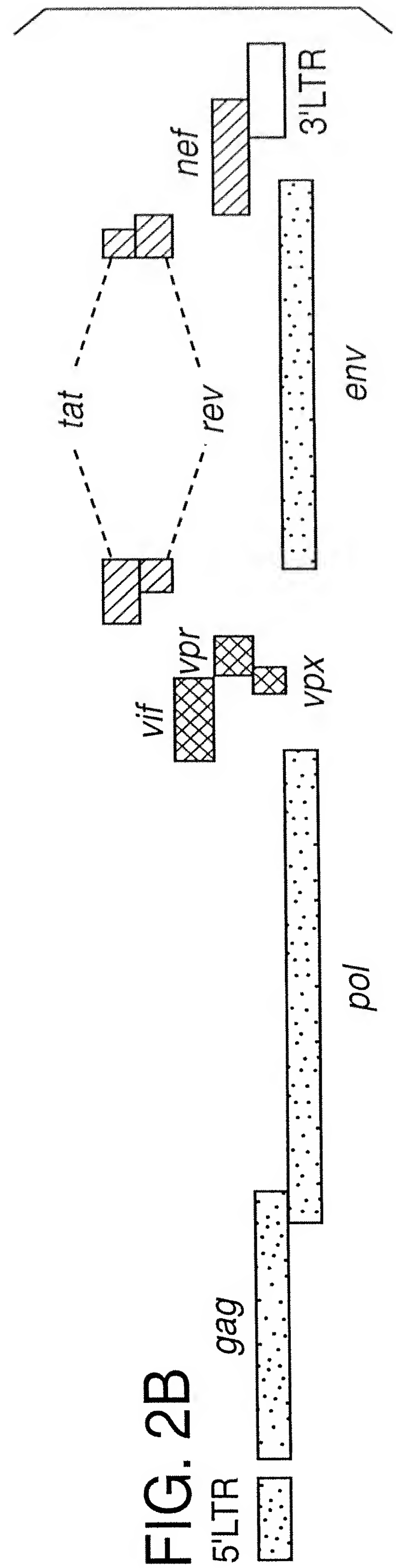

5'LTR
gag
pol
vif
vpr
vpx
tat
rev
env
nef
3'LTR

FIG. 3A

pROD(PK36) Leader Sequence

	310	320	330	340	350
HIV2ROD	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
ROD(PK36)	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
	360	370	380	390	400
HIV2ROD	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
ROD(PK36)	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
	410	420	430	440	450
HIV2ROD	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
ROD(PK36)	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	GAGCGTGTGG	AGCGGGAGGA
	460	470	480	490	500
HIV2ROD	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
ROD(PK36)	GAAAGAGGCT	CCGGGTGAAG	GTAAGTACCT	ACACC	
	510	520	530	540	550
HIV2ROD	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
ROD(PK36)				T	GGGAGATGGG

FIG. 3B

pROD(SK36) Leader Sequence

	310	320	330	340	350
HIV2ROD	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
ROD(SK36)	GTTGG				
	360	370	380	390	400
HIV2ROD	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
ROD(SK36)					
	410	420	430	440	450
HIV2ROD	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
ROD(SK36)					
	460	470	480	490	500
HIV2ROD	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
ROD(SK36)	CT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	510	520	530	540	550
HIV2ROD	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
ROD(SK36)	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG

FIG. 3C

pROD(SD36) Leader Sequence

	310	320	330	340	350
HIV2ROD	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
ROD(SD36)	GTTGG				

	360	370	380	390	400
HIV2ROD	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
ROD(SD36)					

	410	420	430	440	450
HIV2ROD	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
ROD(SD36)					

	460	470	480	490	500
HIV2ROD	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
ROD(SD36)	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	

	510	520	530	540	550
HIV2ROD	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
ROD(SD36)				GT	GGGAGATGGG

FIG. 3D

pROD(CG36) Leader Sequence

(Designed and to be created)

	310	320	330	340	350
HIV2ROD	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
ROD(CG36)	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG

	360	370	380	390	400
HIV2ROD	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
ROD(CG36)	GCTGAGTGAA	GGCAGTAAGG			

	410	420	430	440	450
HIV2ROD	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
ROD(CG36)					

	460	470	480	490	500
HIV2ROD	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
ROD(CG36)	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	

	510	520	530	540	550
HIV2ROD	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
ROD(CG36)				GT	GGGAGATGGG

FIG. 3E

pROD(MR36) Leader Sequence
(Designed and to be created)

	310	320	330	340	350
HIV2ROD	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
ROD(MR36)	GTTGG				

	360	370	380	390	400
HIV2ROD	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
ROD(MR36)			GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC

	410	420	430	440	450
HIV2ROD	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
ROD(MR36)	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	GAGCGTGTGG	AGCGGGAGGA

	460	470	480	490	500
HIV2ROD	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
ROD(MR36)	GAAAGAGGCT	CCGGGTGAAG	GTAAGTACCT	ACACC	

	510	520	530	540	550
HIV2ROD	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
ROD(MR36)				GT	GGGAGATGGG

FIG. 4A

HIV-2 pROD(SD36/EM) Sequence of Mutant Region of Envelope
(Insertion mutant)

ROD	(6351)	ACAGAGGCTT TTGATGCAT
EM		ACAGAGGCTT TTGATGCATA GGTAGCGTGA GATCTTAGTG CA
ROD		G GAATAATA CA (6380)
EM		TAGGTAGC GTGAGATCTT AGTGCAAAGA TCGAATAATA CA

FIG. 4B

pCM-ENV(ROD)(B-14)

```
   1 TCAATATTGG CCATTAGCCA TATTATTCAT TGGTTATATA GCATAAATCA
  51 ATATTGGCTA TTGGCCATTG CATACGTTGT ATCTATATCA TAATATGTAC
 101 ATTTATATTG GCTCATGTCC AATATGACCG CCATGTTGGC ATTGATTATT
 151 GACTAGTTAT TAATAGTAAT CAATTACGGG GTCATTAGTT CATAGCCCAT
 201 ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC GCCTGGCTGA
 251 CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
 301 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC
 351 GGTAAACTGC CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG
 401 CCCCCTATTG ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA
 451 GTACATGACC TTACGGGACT TTCCTACTTG GCAGTACATC TACGTATTAG
 501 TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC CAATGGGCGT
 551 GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT
 601 CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC
 651 GTAATAACCC CGCCCCGTTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG
 701 GAGGTCTATA TAAGCAGAGC TCGTTTAGTG AACCGTCAGA TCACTAGAAG
 751 CTTTATTGCG GTAGTTTATC ACAGTTAAAT TGCTAACGCA GTCAGTGCTT
 801 CTGACACAAC GGTCTCGAAC TTAAGCTGCA GAAGTTGGTC GTGAGGCACT
 851 GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA
 901 ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA
 951 TTGGTCTTAC TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC
1001 CAGTTCAATT ACAGCTCTTA AGGCTAGAGT ACTTAATACG ACTCACTATA
1051 GGCTAGCCTC GA                     TACACCAGAC AAGTGAGTAT 180
GATGAATCAG CTGCTTATTG CCATTTTATT AGCTAGTGCT TGCTTAGTAT ATTGCACCCA 240
ATATGTAACT GTTTTCTATG GCGTACCCAC GTGGAAAAAT GCAACCATTC CCCTCTTTTG 300

        310        320        330        340        350        360
TGCAACCAGA AATAGGGATA CTTGGGGAAC CATACAGTGC TTGCCTGACA ATGATGATTA 360
TCAGGAAATA ACTTTGAATG TAACAGAGGC TTTTGATGCA TGGAATAATA CAGTAACAGA 420
ACAAGCAATG AAAGATGTCT GGCATCTATT CGAGACATCA ATAAAACCAT GTGTCAAACT 480
AACACCTTTA TGTGTAGCAA TGAAATGCAG CAGCACAGAG AGCAGCATAG GGAACAACAC 540
AACCTCAAAG AGCACAAGCA CAACCACAAC CACACCCACA GACCAGGAGC AAgagataag 600

        610        620        630        640        650        660
tgaggatact ccatgcgcac gcgcagacaa ctgctcagga ttgggagagg aagaaacgat 660
caattgccag ttcaatatga caggattaga aagagataag aaaaaacagt ataatgaaac 720
atggtactca aaagatgtgg tttgtgagac aaataatagc acaaatcaga cccagtgtta 780
catgaaccat tgcaacacat cagtcatcac agaatcatgt gacaagcact attgggatgc 840
tataaggttt agatactgtg caccaccggg ttatgcccta ttaagatgta atgataccaa 900
```

FIG. 4C

```
       910       920       930       940       950       960
ttattcaggc tttgcaccca actgttctaa agtagtagct tctacatgca ccaggatgat 960
ggaaacgcaa acttccacat ggtttggctt taatggcact agagcagaga atagaacata 1020
tatctattgg catggcagag ataatagaac tatcatcagc ttaaacaaat attataatct 1080
cagtttgcat tgtaagaggc cagggaataa gatagtgaaa caaataatgc ttatgtcagg 1140
acatgtgttt cactcccact accagccgat caataaaaga cccagacaag catggtgctg 1200
      1210      1220      1230      1240      1250      1260
gttcaaaggc aaatggaaag acgccatgca ggaggtgaag gaaacccttg caaaacatcc 1260
caggtataga ggaaccaatg acacaaggaa tattagcttt gcagcgccag gaaaaggctc 1320
agacccagaa gtagcataca tgtggactaa ctgcagagga gagtttctct actgcaacat 1380
gacttggttc ctcaattgga tagagaataa gacacaccgc aattatgcac cgtgccatat 1440
aaagcaaata attaacacat ggcataaggt agggagaaat gtatatttgc ctcccaggga 1500
      1510      1520      1530      1540      1550      1560
aggggagctg tcctgcaact caacagtaac cagcataatt gctaacattg actggcaaaa 1560
caataatcag acaaacatta cctttagtgc agaggtggca gaactataca gattggagtt 1620
gggagattat aaattggtag aaataacacc aattggcttc gcacctacaa aagaaaaaag 1680
atactcctct gctcacggga gacatacaag aggtgtgttc gtgctagggt tcttgggttt 1740
tctcgcaaca gcaggttctg caatgggcgc ggcgtccctg accgtgtcgg ctcagtcccg 1800
      1810      1820      1830      1840      1850      1860
gactttactg gccgggatag tgcagcaaca gcaacagctg ttggacgtgg tcaagagaca 1860
acaagaactg ttgcgactga ccgtctgggg aacgaaaaac ctccaggcaa gagtcactgc 1920
tatagagaag tacctacagg accaggcgcg gctaaattca tggggatgtg cgtttagaca 1980
agtctgccac actactgtac catgggttaa tgattcctta gcacctgact gggacaatat 2040
gacgtggcag gaatgggaaa aacaagtccg ctacctggag gcaaatatca gtaaaagttt 2100
      2110      2120      2130      2140      2150      2160
agaacaggca caaattcagc aagagaaaaa tatgtatgaa ctacaaaaat taaatagctg 2160
ggatattttt ggcaattggt ttgacttaac ctcctgggtc aagtatattc aatatggagt 2220
gcttataata gtagcagtaa tagctttaag aatagtgata tatgtagtac aaatgttaag 2280
taggcttaga aagggctata ggcctgtttt ctcttcccc  cccggttata tccaacagat 2340
ccatatccac aaggaccggg gacagccagc caacgaagaa acagaagaag acggtggaag 2400
      2410      2420      2430      2440      2450      2460
caacggtgga gacagatact ggccctggcc gatagcaTAT ATACATTTCC TGATCCGCCA 2460
GCTGATTCGC CTCTTGACCA GACTATACAG CATCTGCAGG GACTTACTAT CCAGGAGCTT 2520
CCTGACCCTC CAACTCATCT ACCAGAATCT CAGAGACTGG CTGAGACTTA GAACAGCCTT 2580
CTTGCAATAT GGGTGCGAGT GGATCCAAGA AGCATTCCAG GCCGCCGCGA GGGCTACAAG 2640
AGAGACTCTT GCGGGCGCGT GCAGGGGCTT GTGGAGGGTA TTGGAACGAA TCGGGAGGGG 2700
      2710      2720      2730      2740      2750      2760
AATACTCGCG GTTCCAAGAA GGATCAGACA GGGAGCAGAA ATCGCCTCCT GTGAGGGACG 2760
GCAGTATAGC CAGGGAGACT TTATGAATAC TCCATGG
```

FIG. 4D

GGCGG

1101 CCGCTTCGAG CAGACATGAT AAGATACATT GATGAGTTTG GACAAACCAC
1151 AACTAGAATG CAGTGAAAAA AATGCTTTAT TTGTGAAATT TGTGATGCTA
1201 TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT TAACAACAAC
1251 AATTGCATTC ATTTTATGTT TCAGGTTCAG GGGGAGATGT GGGAGGTTTT
1301 TTAAAGCAAG TAAAACCTCT ACAAATGTGG TAAAATCGAT AAGGATCCGG
1351 GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGTTG
1401 CGCAGCCTGA ATGGCGAATG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG
1451 GCGGGTGTGG TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT
1501 AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG
1551 GCTTTCCCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT

FIG. 4E

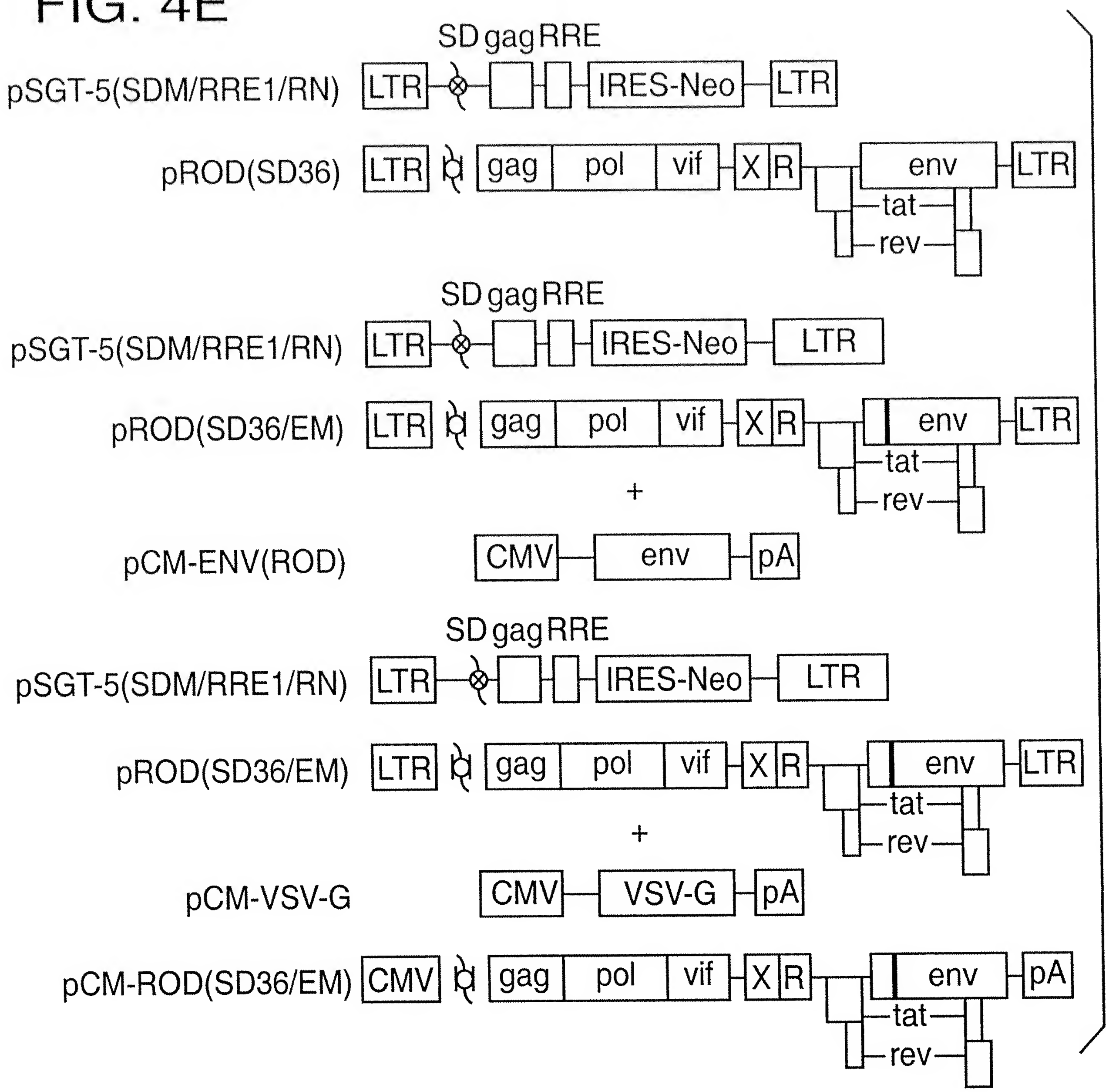

SD gag RRE
pSGT-5(SDM/RRE1/RN)
LTR
IRES-Neo
LTR
pROD(SD36)
LTR
gag
pol
vif
X
R
env
LTR
tat
rev
SD gag RRE
pSGT-5(SDM/RRE1/RN)
LTR
IRES-Neo
LTR
pROD(SD36/EM)
LTR
gag
pol
vif
X
R
env
LTR
tat
rev
+
pCM-ENV(ROD)
CMV
env
pA
SD gag RRE
pSGT-5(SDM/RRE1/RN)
LTR
IRES-Neo
LTR
pROD(SD36/EM)
LTR
gag
pol
vif
X
R
env
LTR
tat
rev
+
pCM-VSV-G
CMV
VSV-G
pA
pCM-ROD(SD36/EM)
CMV
gag
pol
vif
X
R
env
pA
tat
rev

FIG. 5A

SIV 5' LTR Leader Sequence

R→

10	20	30	40	50
GCTCTGTATT	CAGTCGCTCT	GCGGAGAGGC	TGGCAGATTG	AGCCCTGGGA
60	70	80	90	100
GGTTCTCTCC	AGCACTAGCA	GGTAGAGCCT	GGGTGTTCCC	TGCTAGACTC
110	120	130	140	150
TCACCAGCAC	TTGGCCGGTG	CTGGGCAGAG	TGACTCCACG	CTTGCTTGCT
			← R |U5 →	
160	170	180	190	200
TAAAGCCCTC	TTCAATAAAG	CTGCCATTTT	AGAAGTAAGC	TAGTGTGTGT
210	220	230	240	250
TCCCATCTCT	CCTAGCCGCC	GCCTGGTCAA	CTCGGTACTC	AATAATAAGA
260	270	280	290	300
AGACCCTGGT	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	GAAGCAGGAA
← U5 |Leader →				
310	320	330	340	350
AATCCCTAGC	AGATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA
360	370	380	390	400
CTCCTGAGTA	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC
410	420	430	440	450
GACGGAGTGC	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG
		SD		
460	470	480	490	500
CGGGAGAGGA	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA
510	520	530	540	550
ATAGCTGTCT	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG
560				
CGTGAGAAAC				

FIG. 5B

pSIV(SD36)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SD36	GATTGG				
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
SD36					
	420	430	440	450	460
WTL	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SD36					
		SD			
	470	480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
SD36	CTCC	GGTTGCAGGT	AAGTGCAACA	CA	
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAAC
SD36			GT	GGGAGATGGG	CGTGAGAAAC

FIG. 5C

pSIV(SDM)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SDM	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
SDM	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
	420	430	440	450	460
WTL	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SDM	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
		SD			
	470	480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
SDM	AGAGGCCTCC	GGTTGATATC	GAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAAC
SDM	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAAC

FIG. 6A

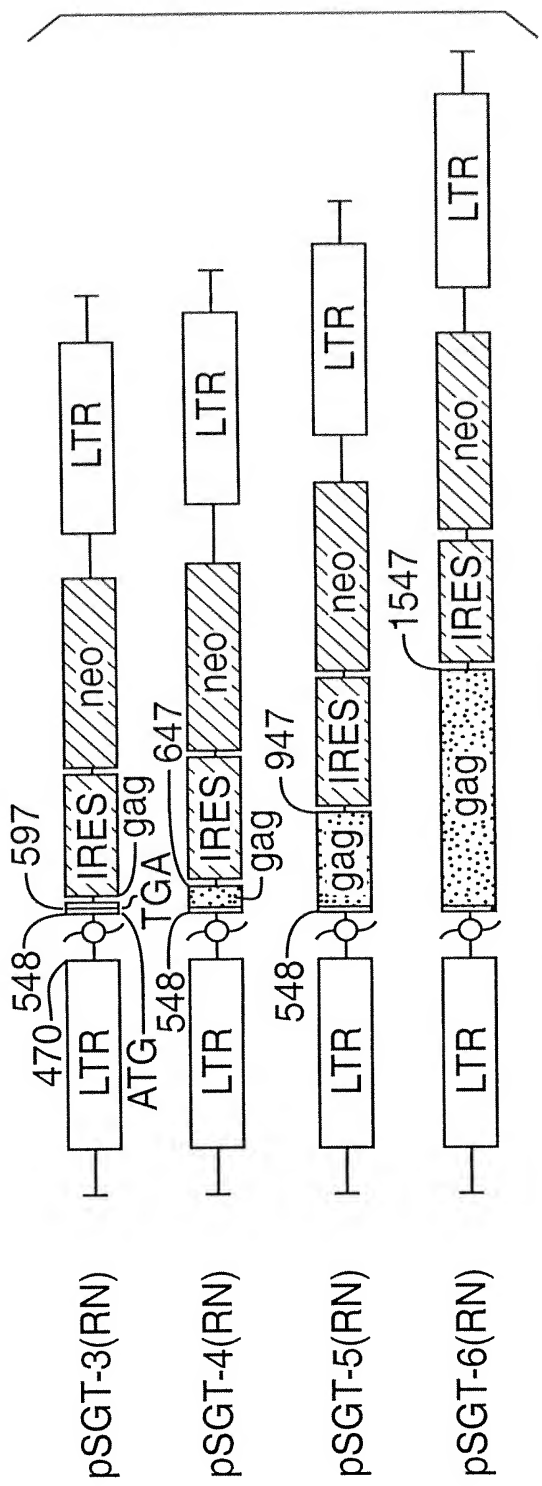

pSGT-3(RN)
pSGT-4(RN)
pSGT-5(RN)
pSGT-6(RN)
LTR
neo
IRES
gag
470
548
597
ATG
TGA
647
947
1547

FIG. 6B

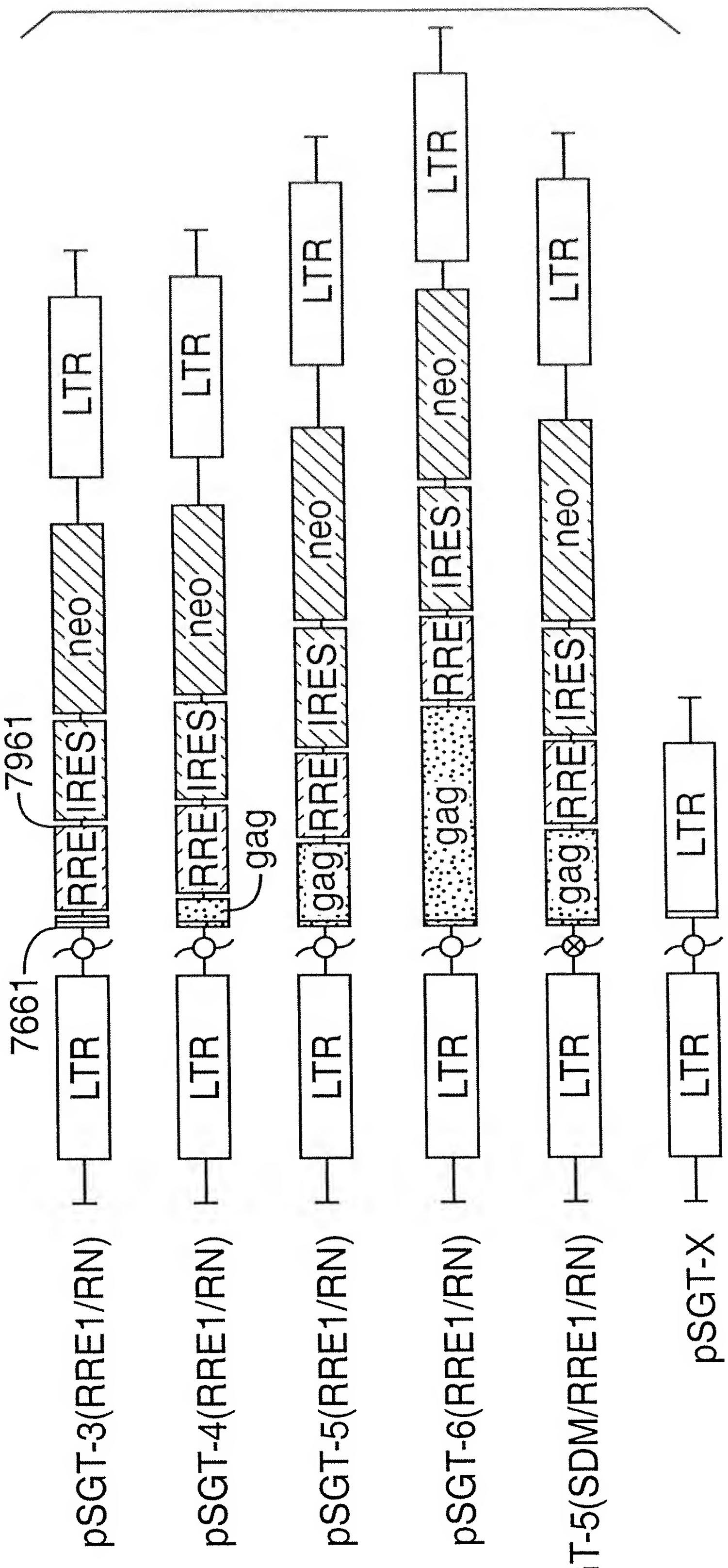

pSGT-3(RRE1/RN)
pSGT-4(RRE1/RN)
pSGT-5(RRE1/RN)
pSGT-6(RRE1/RN)
pSGT-5(SDM/RRE1/RN)
pSGT-X
LTR
neo
IRES
RRE
gag
7661
7961

FIG. 7A

pSGT5(SDM/RR)

|U3 -530 -520
GGAA GGGCTGTATT ACAGTGATAG

-530 -520 -510 -500 -490 -480
GAGACGTAGA GTCCTAGACA TATACTTAGA AAAGGAAGAG GGAATAATTG GAGACTGGCA

-470 -460 -450 -440 -430 -420
GAACTATACT CATG GACCAG GAGTAAGGTA TCCAAAGTTC TTTGGGTGGT TATGGAAGCT

-410 -400 -390 -380 -370 -360
AGTACCAGTA GATGTCCCAC AAGA GGGAGA TGACAGTGAG ACTCACTGCT TAGTGCATCC

-350 -340 -330 -320 -310 -300
AGCA CAAACA AGCAGGTTTG ATGACCCGCA TGGAGAAACA TTAGTTTGGA GGTTTGACCC

-290 -280 -270 -260 -250 -240
CACGCTAGCT TTTAGCTACG AGGCCTTTAT TCGATACCCA GAGGAGTTTG GGTACAAGTC

-230 -220 -210 -200 -190 -180
AGGCCTGCCA GAGGATGAAT GGAAGGCAAG ACTGAAAGCA AGAGGGATAC CGTTAGCTA

-170 -160 -150 -140 -130 -120
AAAACAGGAA CAGCTATACT TGGTCAGGGC AGGAAGTAAC TAACAGAAAA CAGCTGAGAC

-110 -100 -90 -80 -70 -60
TGCAGGGACT TTCCAGAAGG GGCTGTTACC AGGGGAGGGA CATGGGAGGA GCCGGTGGGG

-50 -40 -30 -20 -10 U3|
AACGCCCTCA TACTTTCTGT ATAAATGTAC CCGCTACTCG CATTGTATTC

|R 10 20 30 40 50 60
GTTCGCTCTG CGGAGAGGCT GGCAGATTGA GCCCTGGGAG GTTCTCTCCA GCACTAGCAG

70 80 90 100 110 120
TGGTCACCTG GGTGTTCCCT GCTAGACTCT CACCAGTGCT TGGCCGGCAC TGGGCAGACG

130 140 150 160 170 R|U5 180
GCTCCACGCT TGCTTGCTTA AAAGACCTCT TAATAAAGCT GCCAGTTAGA AGCAAGTTAA

190 200 210 220 230 240
GTGTGTGCTC CCATCTCTCC TAGTCGCCGC CTGGTCATTC GGTGTTCATC TAAAGTAACA

250 260 270 280 290 300
AGACCCTGGT CTGTTAGGAC CCTTTCTGCT TTGGGAAACC AAGGCAGGAA AATCCCTAGC

U5|Leader 310 320 330 340 350 360
AGGTTGGCGC CCGAACAGGG ACTTGAAGAA GACTGAGAAG CCTTGGAACA CGGCTGAGTG

370 380 390 400 410 420
AAGGCAGTAA GGGCGGCAGG AACAAACCAC GACGGAGTGC TCCTAGAAAA GCGCAGGCCG

FIG. 7B

430 440 450 460 470|---SDM---| 480
AGGTACCAAG GGCGGCGTGT GGAGCGGGAG TGAAAGAGGC CTCCGGGTGA TATCAGTGCC

490 500 510 520 530 540
TACACCAAAT ACAGTAGCCA GAAGGGCTTG TTATCCTACC TTTAGACGGG TAGAAGATTG

Leader |gag 560 570 580 590 600
TGGGAGATGC CATGGTAGGG CGCGAGAAAC TCCGTCTTGA GAGGGAAAAA AGCAGACGAA

610 620 630 640 650 660
TTAGAAAAGA TTAGGTTACG GCCCGGCGGA AAGAAAAAAT ATAGGCTAAA ACATATTGTG

670 680 690 700 710 720
TGGGCAGCGA ATGAATTGGA CAGATTCGGA TTGGCAGAGA GCCTGTTGGA GTCAAAAGAG

730 740 750 760 770 780
GGTTGCCAAAA AAATTCTTAC AGTTTTAGAT CCATTAGTAC CGACAGGGTC AGAAAATTTA

790 800 810 820 830 840
AAAAGCCTTT TTAATACTGT CTGCGTCATT TGGTGTATAC ACGCAGAAGA GAAAGCGAAA

850 860 870 880 890 900
GATACTGAAG AAGCAAAACA AAAGGTACAG AGACATCTAG TGGCAGAAAC AAAAACTACA

910 920 930 940 950gag(955) |poly(L)
GAAAAAATGC CAAGTACAAG TAGACCAACA GCACCACCTA GCGGGAACGG AGGAACTCGA

970 980 | RRE(7661) 990 1000 1010 1020
ATGCATGGTG ACCGCGGCCG CAGAGGTGTA TTCGTGCTAG GGTTCTTAGG TTTTCTCACA

1030 1040 1050 1060 1070 1080
GCAGGAGCTG CAATGGGCGC GGCGTCCTTG ACGCTGTCGG CTCAGTCTCG GACTTTATTG

1090 1100 1110 1120 1130 1140
GCCGGGATAG TGCAGCAACA GCAACAGCTG TTGGACGTGG TCAAGAGACA ACAAGAAATG

1150 1160 1170 1180 1190 1200
TTGCGACTGA CCGTCTGGGG AACAAAAAAT CTCCAGGCAA GAGTCACTGC TATCGAGAAA

1210 1220 1230 1240 1250 1260
TACTTAAAGG ACCAGGCGC AACTAAATTCA TGGGGATGTG CGTCTAGACA AGTCTGCCAC

1270 RRE(7960)| poly(L) 1290 |(8770) 1310 1320
ACTACTGTAC CATGGGTAGC GGCCGCTCGC GAGTAGACCA TGGAGAGCCC CAGCAGAAGG

1330 1340 1350 1360 1370 1380
GGAGAAAGGC TCGTACAAGC AACAAAATAT GGATGATGTA GATTCAGATG ATGATGACCT

1390 1400 1410 1420 1430 1440
AGTAGGGGTC CCTGTCACAC CAAGAGTACC ATTAAGAGAA ATGACATATA GGTTGGCAAG

1450 1460 1470 (8944)|U3 1480 1490 1500
AGAT ATGTCA CATTTGATAA AAGAAAAGGG GGGACTGGAA GGGCTGTATT ACAGTGATAG

FIG. 7C

```
        1510        1520        1530        1540        1550        1560
GAGACGTAGA  GTCCTAGACA  TATACTTAGA  AAAGGAAGAG  GGAATAATTG  GAGACTGGCA

        1570        1580        1590        1600        1610        1620
GAACTATACT  CATG GACCAG  GAGTAAGGTA  TCCAAAGTTC  TTTGGGTGGT  TATGGAAGCT

        1630        1640        1650        1660        1670        1680
AGTACCAGTA  GATGTCCCAC  AAGA GGGAGA  TGACAGTGAG  ACTCACTGCT  TAGTGCATCC

        1690        1700        1710        1720        1730        1740
AGCA CAAACA  AGCAGGTTTG  ATGACCCGCA  TGGAGAAACA  TTAGTTTGGA  GGTTTGACCC

        1750        1760        1770        1780        1790        1800
CACGCTAGCT  TTTAGCTACG  AGGCCTTTAT  TCGATACCCA  GAGGAGTTTG  GGTACAAGTC

        1810        1820        1830        1840        1850        1860
AGGCCTGCCA  GAGGATGAAT  GGAAGGCAAG  ACTGAAAGCA  AGAGGGATAC  CGTTAGCTA

        1870        1880        1890        1900        1910        1920
AAAACAGGAA  CAGCTATACT  TGGTCAGGGC  AGGAAGTAAC  TAACAGAAAA  CAGCTGAGAC

        1930        1940        1950        1960        1970        1980
TGCAGGGACT  TTCCAGAAGG  GGCTGTTACC  AGGGGAGGGA  CATGGGAGGA  GCCGGTGGGG

        1990        2000        2010        2020        U3|R        2040
AACGCCCTCA  TACTTTCTGT  ATAAATGTAC  CCGCTACTCG  CATTGTATTC  AGTCGCTCTG

        2050        2060        2070        2080        2090        2100
CGGAGAGGCT  GGCAGATTGA  GCCC TGGGAG  GTTCTCTCCA  GCACTAGCAG  GTAGGCCTG

        2110        2120        2130        2140        2150        2160
GGTGTTCCCT  GCTAGACTCT  CACCAGTGCT  TGGCCGGCAC  TGGGCAGACG  GCTCCACGCT

        2170        2180        2190        R|
TGCTTGCTTA  AAAGACCTCT  TAATAAAGC  TGCCA
```

FIG. 7D

10	20	30	40	50	60
TCTAGAGGAA	TTCCGCCCCT	CTCCCTCCCC	CCCCCCTAAC	GTTACTGGCC	GAAGCCGCTT
70	80	90	100	110	120
GGAATAAGGC	CGGTGTGCGT	TTGTCTATAT	GTTATTTTCC	ACCATATTGC	CGTCTTTTGG
130	140	150	160	170	180
CAATGTGAGG	GCCCGGAAAC	CTGGCCCTGT	CTTCTTGACG	AGCATTCCTA	GGGGTCTTTC
190	200	210	220	230	240
CCCTCTCGCC	AAAGGAATGC	AAGGTCTGTT	GAATGTCGTG	AAGGAAGCAG	TTCCTCTGGA
250	260	270	280	290	300
AGCTTCTTGA	AGACAAACAA	CGTCTGTAGC	GACCCTTTGC	AGGCAGCGGA	ACCCCCCACC
310	320	330	340	350	360
TGGCGACAGG	TGCCTCTGCG	GCCAAAAGCC	ACGTGTATAA	GATACACCTG	CAAAGGCGGC
370	380	390	400	410	420
ACAACCCCAG	TGCCACGTTG	TGAGTTGGAT	AGTTGTGGAA	AGAGTCAAAT	GGCTCTCCTC
430	440	450	460	470	480
AAGCGTATTC	AACAAGGGGC	TGAAGGATGC	CCAGAAGGTA	CCCCATTGTA	TGGGATCTGA
490	500	510	520	530	540
TCTGGGGCCT	CGGTGCACAT	GCTTTACATG	TGTTTAGTCG	AGGTTAAAAA	ACGTCTAGGC
550	560	570	580	590	600
CCCCCGAACC	ACGGGGACGT	GGTTTTCCTT	TGAAAAACAC	GATGATAAGC	TTGCCACAAC
610	620	630	640	650	660
CATGGCTGAA	CAAGATGGAT	TGCACGCAGG	TTCTCCGGCC	GCTTGGGTGG	AGAGGCTATT
670	680	690	700	710	720
CGGCTATGAC	TGGGCACAAC	AGACAATCGG	CTGCTCTGAT	GCCGCCGTGT	TCCGGCTGTC
730	740	750	760	770	780
AGCGCAGGGG	CGCCCGGTTC	TTTTTGTCAA	GACCGACCTG	TCCGGTGCCC	TGAATGAACT
790	800	810	820	830	840
GCAGGACGAG	GCAGCGCGGC	TATCGTGGCT	GGCCACGACG	GGCGTTCCTT	GCGCAGCTGT
850	860	870	880	890	900
GCTCGACGTT	GTCACTGAAG	CGGGAAGGGA	CTGGCTGCTA	TTGGGCGAAG	TGCCGGGGCA
910	920	930	940	950	960
GGATCTCCTG	TCATCTCACC	TTGCTCCTGC	CGAGAAAGTA	TCCATCATGG	CTGATGCAAT
970	980	990	1000	1010	1020
GCGGCGGCTG	CATACGCTTG	ATCCGGCTAC	CTGCCCATTC	GACCACCAAG	CGAAACATCG
1030	1040	1050	1060	1070	1080
CATCGAGCGA	GCACGTACTC	GGATGGAAGC	CGGTCTTGTC	GATCAGGATG	ATCTGGACGA
1090	1100	1110	1120	1130	1140
AGAGCATCAG	GGGCTCGCGC	CAGCCGAACT	GTTCGCCAGG	CTCAAGGCGC	GCATGCCCGA
1150	1160	1170	1180	1190	1200
CGGCGAGGAT	CTCGTCGTGA	CCCATGGCGA	TGCCTGCTTG	CCGAATATCA	TGGTGGAAAA
1210	1220	1230	1240	1250	1260
TGGCCGCTTT	TCTGGATTCA	TCGACTGTGG	CCGGCTGGGT	GTGGCGGACC	GCTATCAGGA
1270	1280	1290	1300	1310	1320
CATAGCGTTG	GCTACCCGTG	ATATTGCTGA	AGAGCTTGGC	GGCGAATGGG	CTGACCGCTT
1330	1340	1350	1360	1370	1380
CCTCGTGCTT	TACGGTATCG	CCGCTCCCGA	TTCGCAGCGC	ATCGCCTTCT	ATCGCCTTCT
1390	1400	1410			
TGACGAGTTC	TTCTGAGCGG	GATCGGCTAG	C		

FIG. 7E

pSGT-5(SDM) 5'LTR-Leader Sequence

```
                     10          20          30          40          50
HIV2ST       GTTCGCTCTG  CGGAGAGGCT  GGCAGATTGA  GCCCTGGGAG  GTTCTCTCCA
pSGT5(SDM)   GTTCGCTCTG  CGGAGAGGCT  GGCAGATTGA  GCCCTGGGAG  GTTCTCTCCA

                     60          70          80          90         100
HIV2ST       GCACTAGCAG  TGGTCACCTG  GGTGTTCCCT  GCTAGACTCT  CACCAGTGCT
pSGT5(SDM)   GCACTAGCAG  TGGTCACCTG  GGTGTTCCCT  GCTAGACTCT  CACCAGTGCT

                    110         120         130         140         150
HIV2ST       TGGCCGGCAC  TGGGCAGACG  GCTCCACGCT  TGCTTGCTTA  AAAGACCTCT
pSGT5(SDM)   TGGGCGGCAC  TGGGCAGACG  GCTCCACGCT  TGCTTGCTTA  AAAGACCTCT

                    160         170         180         190         200
HIV2ST       TAATAAAGCT  GCCAGTTAGA  AGCAAGTTAA  GTGTGTGCTC  CCATCTCTCC
pSGT5(SDM)   TAATAAAGCT  GCCAGTTAGA  AGCAAGTTAA  GTGTGTGCTC  CCATCTCTCC

                    210         220         230         240         250
HIV2ST       TAGTCGCCGC  CTGGTCATTC  GGTGTTCATC  TAAAGTAACA  AGACCCTGGT
pSGT5(SDM)   TAGTCGCCGC  CTGGTCATTC  GGTGTTCATC  TAAAGTAACA  AGACCCTGGT

                    260         270         280         290         300
HIV2ST       CTGTTAGGAC  CCTTTCTGCT  TTGGGAAACC  AAGGCAGGAA  AATCCCTAGC
pSGT5(SDM)   CTGTTAGGAC  CCTTTCTGCT  TTGGGAAACC  AAGGCAGGAA  AATCCCTAGC

                    310         320         330         340         350
HIV2ST       AGGTTGGCGC  CCGAACAGGG  ACTTGAAGAA  GACTGAGAAG  CCTTGGAACA
pSGT5(SDM)   AGGTTGGCGC  CCGAACAGGG  ACTTGAAGAA  GACTGAGAAG  CCTTGGAACA

                    360         370         380         390         400
HIV2ST       CGGCTGAGTG  AAGGCAGTAA  GGGCGGCAGG  AACAAACCAC  GACGGAGTGC
pSGT5(SDM)   CGGCTGAGTG  AAGGCAGTAA  GGGCGGCAGG  AACAAACCAC  GACGGAGTGC

                    410         420         430         440         450
HIV2ST       TCCTAGAAAA  GCGCAGGCCG  AGGTACCAAG  GGCGGCGTGT  GGAGCGGGAG
pSGT5(SDM)   TCCTAGAAAA  GCGCAGGCCG  AGGTACCAAG  GGCGGCGTGT  GGAGCGGGAG

                    460         470         480         490         500
HIV2ST       TGAAAGAGGC  CTCCGGGTGA  AGGTAAGTGC  CTACACCAAA  TACAGTAGCC
pSGT5(SDM)   TGAAAGAGGC  CTCCGGGTGA  TATC AGTGC  CTACACCAAA  TACAGTAGCC

                    510         520         530         540         550
HIV2ST       AGAAGGGCTT  GTTATCCTAC  CTTTAGACGG  GTAGAAGATT  GTGGGAGATG
pSGT5(SDM)   AGAAGGGCTT  GTTATCCTAC  CTTTAGACGG  GTAGAAGATT  GTGG AGATG
```

FIG. 7F

pSGT-5(SDM) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA

	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC

	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG

	460	SD 470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	*AGGTA*AGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	*TATC* AGTGC	CTACACCAAA	TACAGTAGCC

	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7G

pSGT-5(SDX) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDX)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA

	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDX)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC

	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDX)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG

	460	SD 470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDX)	TGAAAGAGGC	CTCCGG	GC	CTACACCAAA	TACAGTAGCC

	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDX)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 8

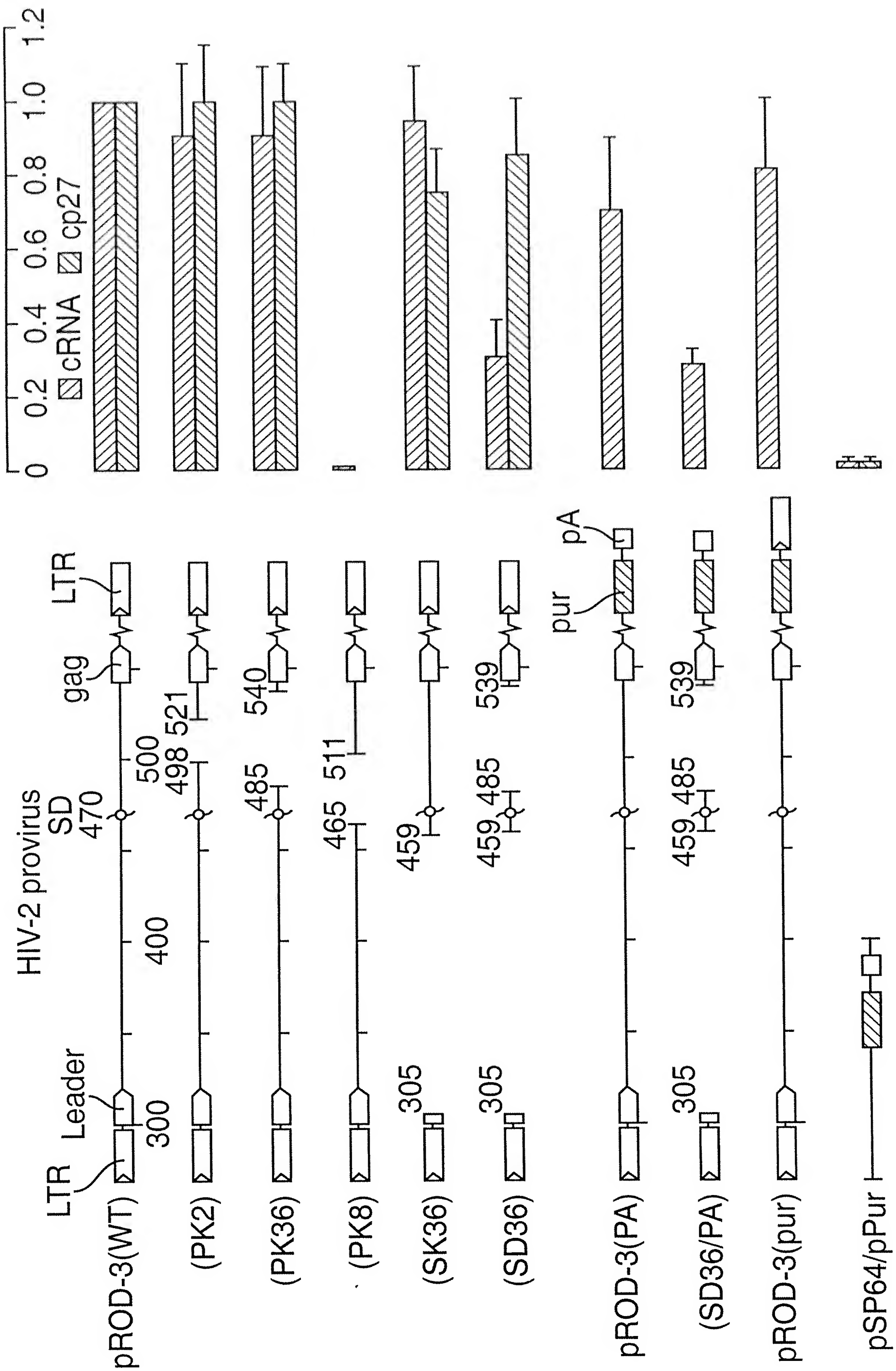

HIV-2 provirus
LTR
Leader
SD
gag
pur
pA
300
400
470
500
498
521
540
485
465
511
459
539
305
pROD-3(WT)
(PK2)
(PK36)
(PK8)
(SK36)
(SD36)
pROD-3(PA)
(SD36/PA)
pROD-3(pur)
pSP64/pPur
Relative expression
cRNA
cp27
0
0.2
0.4
0.6
0.8
1.0
1.2

FIG. 9

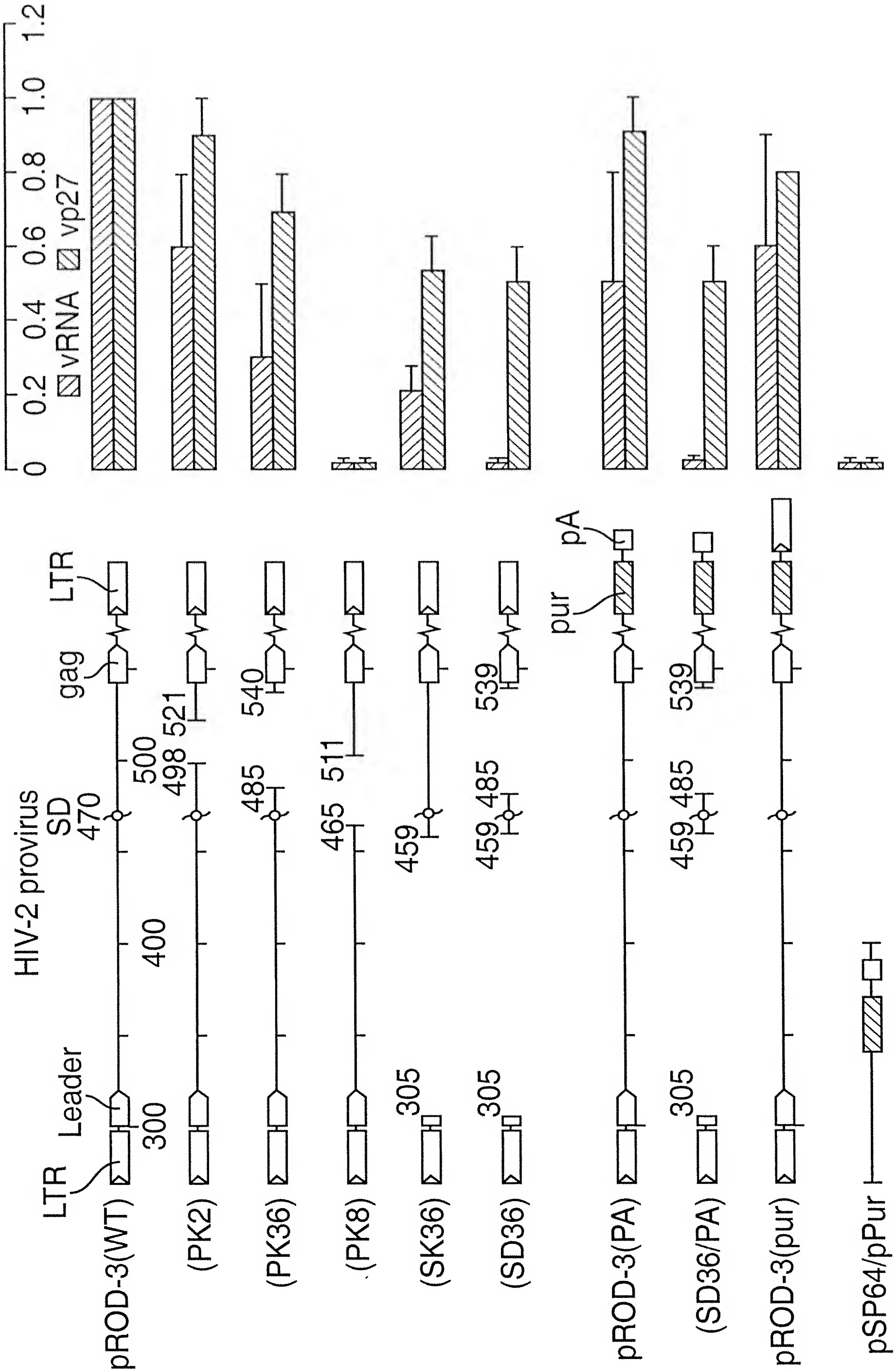

HIV-2 provirus
LTR
Leader
SD
gag
LTR
pur
pA
300
400
470
500
498
521
485
540
465
511
459
305
539
pROD-3(WT)
(PK2)
(PK36)
(PK8)
(SK36)
(SD36)
pROD-3(PA)
(SD36/PA)
pROD-3(pur)
pSP64/pPur
Relative expression
vRNA
vp27
0
0.2
0.4
0.6
0.8
1.0
1.2

FIG. 10

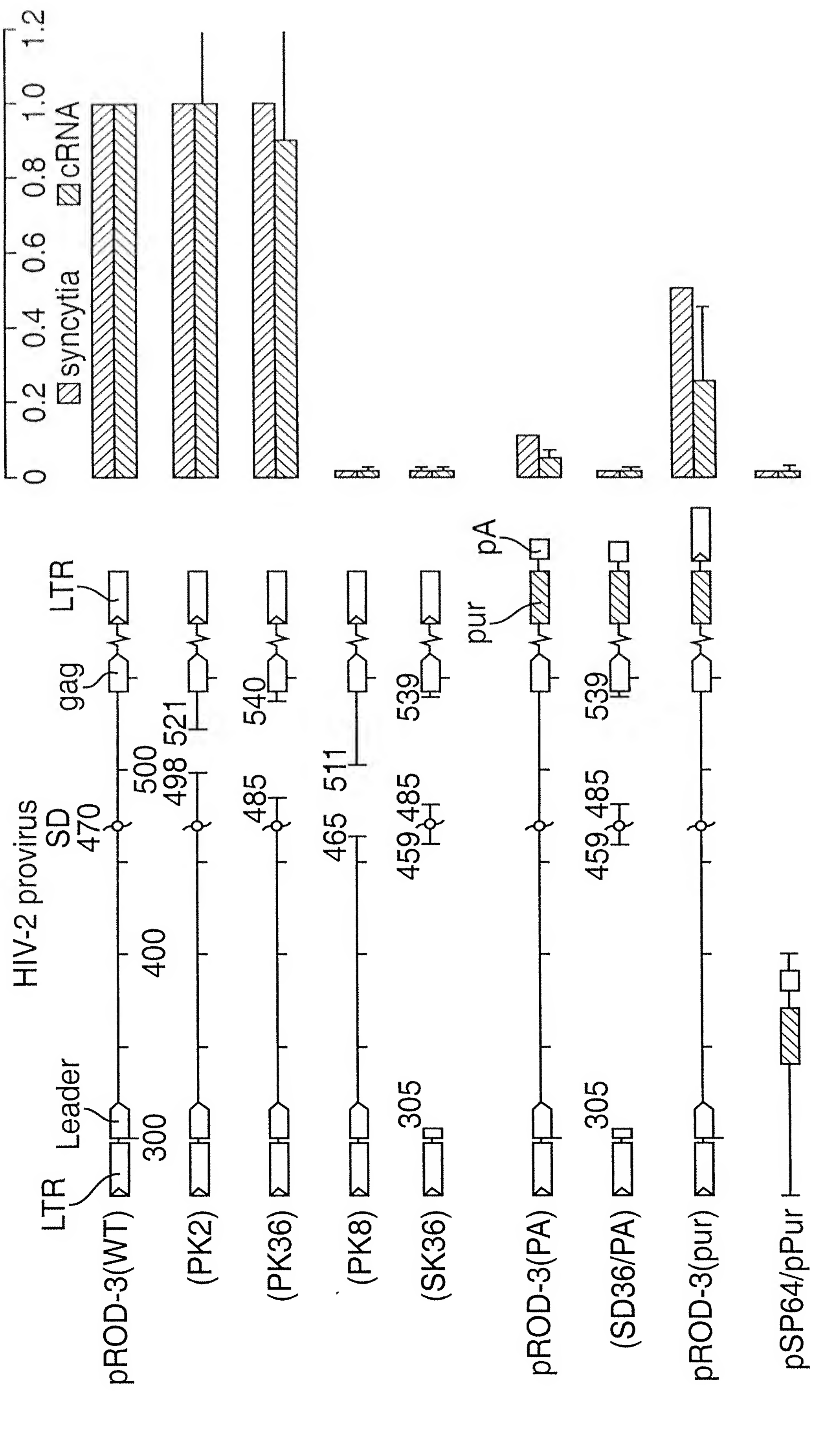
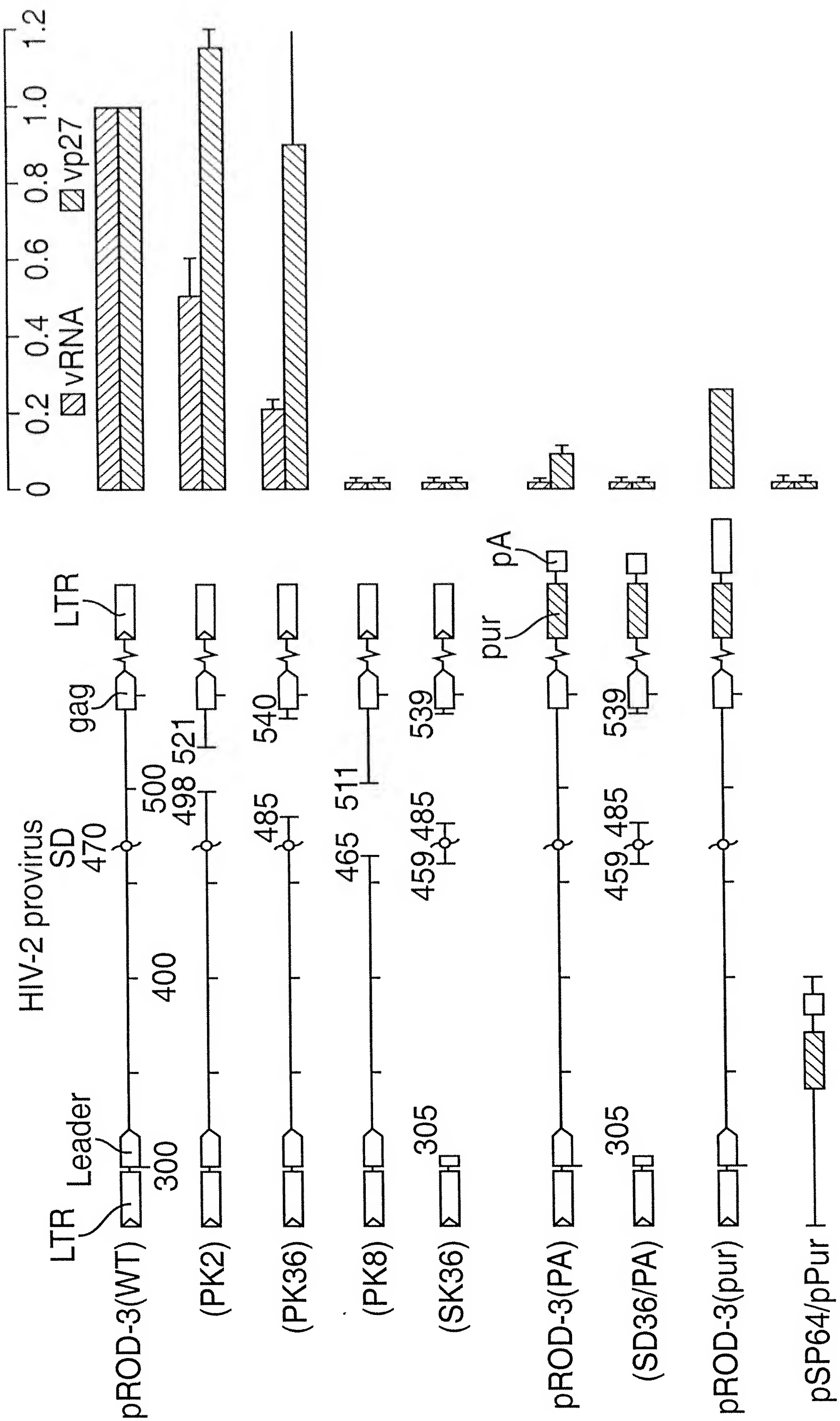

HIV-2 provirus
LTR
Leader
SD
gag
LTR
pur
pA
300
400
470
500
305
498
521
485
540
465
511
459
539
pROD-3(WT)
(PK2)
(PK36)
(PK8)
(SK36)
pROD-3(PA)
(SD36/PA)
pROD-3(pur)
pSP64/pPur
Relative expression
syncytia
cRNA
0
0.2
0.4
0.6
0.8
1.0
1.2

FIG. 11


HIV-2 provirus
LTR
Leader
SD
gag
pur
pA
300
400
470
500
498
521
485
540
465
511
459
485
539
305
pROD-3(WT)
(PK2)
(PK36)
(PK8)
(SK36)
pROD-3(PA)
(SD36/PA)
pROD-3(pur)
pSP64/pPur
Relative expression
vRNA
vp27
0
0.2
0.4
0.6
0.8
1.0
1.2

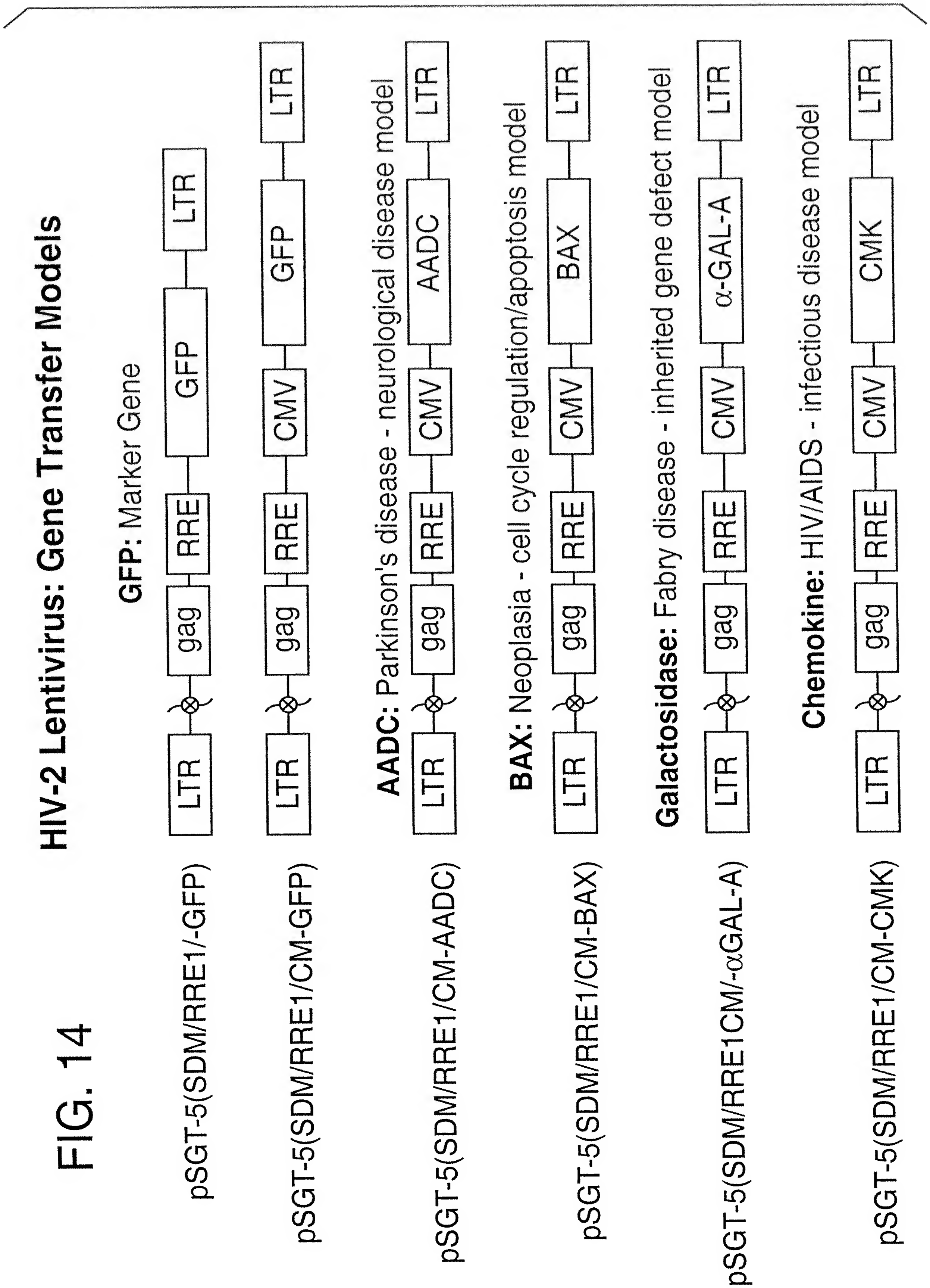

HIV-2 Lentivirus: Gene Transfer Models
GFP: Marker Gene
pSGT-5(SDM/RRE1/-GFP)
LTR gag RRE GFP LTR
pSGT-5(SDM/RRE1/CM-GFP)
LTR gag RRE CMV GFP LTR
AADC: Parkinson's disease - neurological disease model
pSGT-5(SDM/RRE1/CM-AADC)
LTR gag RRE CMV AADC LTR
BAX: Neoplasia - cell cycle regulation/apoptosis model
pSGT-5(SDM/RRE1/CM-BAX)
LTR gag RRE CMV BAX LTR
Galactosidase: Fabry disease - inherited gene defect model
pSGT-5(SDM/RRE1CM/-αGAL-A)
LTR gag RRE CMV α-GAL-A LTR
Chemokine: HIV/AIDS - infectious disease model
pSGT-5(SDM/RRE1/CM-CMK)
LTR gag RRE CMV CMK LTR

FIG. 14